

## SEQUENCE LISTING

- <110> Lebrun, Michel Sailland, Alain Freyssinet, Georges DeGryse, Eric
- <120> Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase, Gene Coding for Said Protein and Transformed Plants Containing Said Gene
- <130> 5500-13
- <140> 08/945,144
- <141> 1998-01-20
- <150> PCT/FR96/01125
- <151> 1996-07-18
- <150> FRANCE 95/08979
- <151> 1995-07-19
- <160> 5
- <170> PatentIn Ver. 2.0
- <210> 1
- <211> 1713
- <212> DNA
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ggc acc Gly Thr	_	_	_	_				_							98
cta ctc Leu Leu					-										146
aac agt Asn Ser		_	_			_			_	_					194
ctc tct Leu Ser 65						-			-	-	_	_	_		242
tgt ggt Cys Gly 80												-	_		290
ttc ttg Phe Leu			_			_	_			_		-	-	-	338
act gct Thr Ala	_				-					-		-		-	386
atg agg Met Arg						_	_	-	_		-	-	_		434
ggt gca Gly Ala 145			-	_					_	_			-	_	482
gtc aat Val Asn 160															530

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					Tyr					_	_	-	-		_	3.0
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Ala	Leu	Gly	Asp 195		Glu	Ile	Glu	Ile 200	Ile	Asp	Lys	Leu	Ile 205	Ser	Ile	
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Ата	225	HIS	ser	Asp	Ser	230	Asp	Arg	Pne	Tyr	235	гÀг	GTÀ	стА	GIN	
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Lys 240	_	ьуs	Ser	Pro	Lys 245	Asn	Ala	Tyr	Val	G1u 250	GIY	Asp	Ala	Ser	Ser 255	
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Ala	Ser	Tyr	Phe	Leu 260	Ala	Gly	Ala	Ala	11e 265	Thr	Gly	Gly	Thr	Val 270	Thr	
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Val	Glu	Gly	Cys 275	Gly	Thr	Thr	Ser	Leu 280	Gln	Gly	Asp	Val	Lys 285	Phe	Ala	
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Glu	Val	Leu 290	Glu	Met	Met	Gly	Ala 295	Lys	Val	Thr	Trp	Thr 300	Glu	Thr	Ser	
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Val	305	Val	Thr	GLY	Pro	910 310	Arg	Glu	Pro	Phe	Gly 315	Arg	Lys	His	Leu	
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320	AIA	iie	Asp	vaı	Asn 325	Met	Asn	гàг	Met	330	Asp	Val	Ala	Met	335	
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Val	Ala	Ser	Trp 355	Arg	Val	Lys	Glu	Thr 360	Glu	Arg	Met	Val	Ala 365	Ile	Arg	•

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_			_	_	ccg Pro		-	-			_			_	_	1202
					atg Met 405											1250
	-		_		atc Ile		_			_			_			1298
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Arg Glu 130	Arg Pro	Ile Gly	Asp 135	Leu	Val	Val	Gly	Leu 140	Lys	Gln	Leu	Gly
Ala Asp 145	Val Asp	Cys Phe		Gly	Thr	Asp	Cys 155	Pro	Pro	Val	Arg	Val 160
Asn Gly	Ile Gly	Gly Leu 165	Pro	Gly	Gly	Lys 170	Val	Lys	Leu	Ser	Gly 175	Ser
Ile Ser	Ser Gln 180	Tyr Leu	Ser	Ala	Leu 185	Leu	Met	Ala	Ala	Pro 190	Leu	Ala
Leu Gly	Asp Val	Glu Ile	Glu	Ile 200	Ile	Asp	Lys	Leu	Ile 205	Ser	Ile	Pro
Tyr Val 210	Glu Met	Thr Leu	Arg 215	Leu	Met	Glu	Arg	Phe 220	Gly	Val	Lys	Ala
Glu His 225	Ser Asp	Ser Trp 230		Arg	Phe	Tyr	Ile 235	Lys	Gly	Gly	Gln	Lys 240
Tyr Lys	Ser Pro	Lys Asn 245	Ala	Tyr	Val	Glu 250	Gly	Asp	Ala	Ser	Ser 255	Ala
Ser Tyr	Phe Leu 260	Ala Gly	Ala	Ala	Ile 265	Thr	Gly	Gly	Thr	Val 270	Thr	Val
Glu Gly	Cys Gly 275	Thr Thr	Ser	Leu 280	Gln	Gly	Asp	Val	Lys 285	Phe	Ala	Glu
Val Leu 290	Glu Met	Met Gly	Ala 295	Lys	Val	Thr	Trp	Thr 300	Glu	Thr	Ser	Val
Thr Val	Thr Gly	Pro Pro 310	Arg	Glu	Pro	Phe	Gly 315	Arg	Lys	His	Leu	Lys 320
Ala Ile	Asp Val	Asn Met 325	Asn	Lys	Met	Pro 330	Asp	Val	Ala	Met	Thr 335	Leu
Ala Val	Val Ala 340	Leu Phe	Ala	Asp	Gly 345	Pro	Thr	Ala	Ile	Arg 350	Asp	Val
Ala Ser	Trp Arg	Val Lys	Glu	Thr 360	Glu	Arg	Met	Val	Ala 365	Ile	Arg	Thr

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys 370 375 380 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr 385 390 395 400 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu 405 410 415 Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro 420 425 430 Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn 435 440 <210> 4 <211> 1340 <212> DNA <213> Zea mays <220> <221> CDS <222> (6)..(1337) <400> 4 ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50 Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser 5 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu 20 25 30 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu 35 40 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly 50 55 60 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtc ggc 242 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Gly 65 . 70 75

tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc

290

Cys 80	Gly	Gly	Lys	Phe	Pro 85	Val	Glu	Asp	Ala	Lys 90	Glu	Glu	Val	Gln	Leu 95	
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				gga Gly												386
				ccc Pro												434
	_	_	_	gat Asp	_					-						482
-				gga Gly						_	_	_	_			530
		-	-	cag Gln 180												578
				gtg Val												626
		_	_	atg Met		_	_	_	_		_					674
				gat Asp												722
		_		cct Pro			_		_	_		_	_		_	770
				ttg Leu 260												818
gtg	gaa	ggt	tgt	ggc	acc	acc	agt	ttg	cag	ggt	gat	gtg	aag	ttt	gct	866
							8									

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Val	Glu	Gly	Cys 275	Gly	Thr	Thr	Ser	Leu 280	Gln	Gly	Asp	Val	Lys 285	Phe	Ala	
	-	_		-	atg Met			_	-						_	914
_		-			cca Pro	_										962
_			-	-	aac Asn 325	_		_	_		_	-	-	_		1010
	-		_	-	ctc Leu		_	_		_		_		_	_	1058
	_			_	gta Val	_					_	-				1106
_				_	ctg Leu		_		_		_		_	_		1154
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	-	-			atg Met 405		-	-				-	_	-	-	1250
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Leu	Ala	Ala 35	Leu	Ser	Glu	Gly	Thr 40	Thr	Val	Val	Asp	Asn 45	Leu	Leu	Asn
Ser	Glu 50	Asp	Val	His	Tyr	Met 55	Leu	Gly	Ala	Leu	Arg 60	Thr	Leu	Gly	Leu
Ser 65	Val	Glu	Ala	Asp	Lys 70	Ala	Ala	Lys	Arg	Ala 75	Val	Val	Val	Gly	Cys 80
Gly	Gly	Lys	Phe	Pro 85	Val	Glu	Asp	Ala	Lys 90	Glu	Glu	Val	Gln	Leu 95	Phe
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Ala	Ala	Gly 115	Gly	Asn	Ala	Thr	Tyr 120	Val	Leu	Asp	Gly	Val 125	Pro	Arg	Met
Arg	Glu 130	Arg	Pro	Ile	Gly	Asp 135	Leu	Val	Val	Gly	Leu 140	Lys	Gln	Leu	Gly
Ala 145	Asp	Val	Asp	Cys	Phe 150	Leu	Gly	Thr	Asp	Cys 155	Pro	Pro	Val	Arg	Val 160
Asn	Gly	Ile	Gly	Gly 165	Leu	Pro	Gly	Gly	Lys 170	Val	Lys	Leu	Ser	Gly 175	Ser
Ile	Ser	Ser	Gln 180	Tyr	Leu	Ser	Ala	Leu 185	Leu	Met	Ala	Ala	Pro 190	Leu	Ala
Leu	Gly	Asp 195	Val	Glu	Ile	Glu	Ile 200	Ile	Asp	Lys	Leu	Ile 205	Ser	Ile	Pro
Tyr	Val 210	Glu	Met	Thr	Leu	Arg 215	Leu	Met	Glu	Arg	Phe 220	Gly	Val	Lys	Ala
Glu 225	His	Ser	Asp	Ser	Trp 230	Asp	Arg	Phe	Tyr	Ile 235	Lys	Gly	Gly	Gln	Lys 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val 

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu 285/

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr/Glu Thr Ser Val 30Ó 

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Glý Arg Lys His Leu Lys 15

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu 

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val 

Ala Ser Trp Arg Val Lys Glu/Thr Glu Arg Met Val Ala Ile Arg Thr 

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys 

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr 

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu 

Val Pro Nal Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro 

Asp/Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn